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Passive sampling reveals composition of airborne bacteria and fungi across five East African cities



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Airborne microbes significantly influence environmental processes and human exposure, yet they remain poorly characterized in Africa. This study presents a regional survey of airborne bacterial and fungal communities across 10 sites in five East African countries: Burundi, the Democratic Republic of the Congo, Kenya, Rwanda, and Tanzania. Polyurethane foam passive air samplers (PUF-PASs) were deployed concurrently, and airborne bacterial and fungal communities were characterized using 16S rRNA gene and ITS amplicon sequencing. Genus-level analyses identified both bacterial taxa (*Massilia*, *Sphingomonas*, *Pseudomonas*, *Bacillus*, and *Kocuria*) and fungal genera (*Cladosporium*, *Alternaria*, *Aspergillus*, *Curvularia*, and *Penicillium*) that are commonly detected in outdoor air and urban atmospheric environments. Beta-diversity analysis revealed no significant country-level differences in bacterial communities (ANOSIM ($R = -0.045$, $p = 0.597$)), while fungal communities exhibited significant differences among countries (ANOSIM ($R = 0.652$, $p = 0.002$)). Cross-border comparisons showed that nearby sites within 10 km did not consistently share similar microbial profiles. These findings indicate a broadly shared regional bacterial aerobiome, with more pronounced spatial structuring among fungal communities. This study serves as a proof-of-concept demonstration that PUF-PASs can be used to characterize airborne microbial communities in East Africa, while highlighting the need for future bioaerosol research with enhanced temporal replication and broader spatial coverage to support long-term public health surveillance in the African region.

Bioaerosols, which include airborne bacteria and fungi, are significant components of atmospheric particulate matter and influence ecosystem processes, agriculture, climate interactions, and human health^{1–4}. Recent advancements in culture-independent sequencing technologies have demonstrated that atmospheric microbial communities are diverse, dynamic, and shaped by local environmental conditions, land use, vegetation, and meteorological factors^{5–9}. Despite the increasing interest in atmospheric microbiology, most studies have focused on Europe, North America, and Asia, leaving significant geographic knowledge gaps in Africa⁸. East

Africa is characterized by rapid urbanization, population growth, diverse climatic zones, extensive freshwater systems, and active volcanic regions, all of which may influence airborne microbial communities¹⁰. Concurrently, the region faces considerable challenges in air pollution monitoring and environmental surveillance due to limited infrastructure and sparse monitoring networks^{11–14}. Although several studies have investigated airborne microorganisms in South Africa, Ghana, and Nigeria, these efforts were typically site-specific and predominantly relied on culture-based methods, which capture only a fraction of the airborne microbial diversity^{15–17}.

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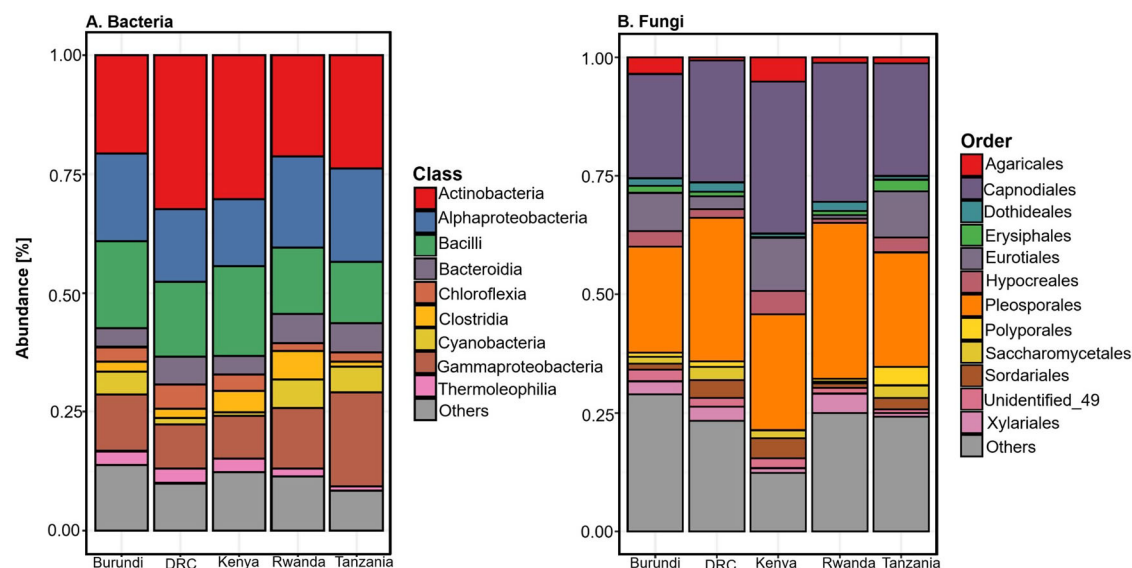


Fig. 1 | Relative abundance of airborne microorganism. Bacterial taxa (A) and fungal taxa (B) in five East African countries at the class level for bacteria and the order level for fungi.

Recently, culture-independent sequencing approaches have been used to characterize airborne microbial communities in Rwanda, highlighting the feasibility of molecular analyses in African contexts^{18,19}. However, regional-scale data on the composition of airborne bacterial and fungal communities remain extremely limited.

Polyurethane Foam Passive Air Samplers (PUF-PASs) offer a practical solution for large-scale environmental monitoring, as they operate without electricity, require minimal maintenance, and can be deployed in remote or resource-limited settings^{20,21}. Prior studies have validated their effectiveness in monitoring both chemical pollutants and airborne microbial communities^{18,22}.

Their low cost and ease of deployment make them particularly well-suited to enhancing environmental monitoring networks across Africa.

In this study, PUF-PASs were deployed simultaneously across East Africa as a proof of concept to (1) characterize airborne bacterial and fungal communities and (2) evaluate whether spatial proximity predicts similarity in microbial community composition across neighboring cross-border locations. This study is the first regional-scale assessment of airborne microbial communities in East Africa using passive sampling and establishes a baseline for future aerobiome monitoring initiatives.

Results and discussion

Microbial community composition

Analysis of microbial community composition revealed both shared and distinct taxonomic patterns across East Africa (Fig. 1). At the bacterial class level, Actinobacteria, Alphaproteobacteria, and Bacilli were the dominant groups across all countries, collectively accounting for the majority of the bacterial community (Fig. 1A). Other classes, including Gammaproteobacteria, Bacteroidia, Chloroflexia, and Clostridia, were also detected but contributed smaller proportions. These bacterial classes are frequently reported in atmospheric environments and include taxa associated with soil, vegetation, aquatic environments, and human activities^{6,7,9,18,19,23,24}.

Fungal communities were primarily composed of members of the orders Pleosporales, Eurotiales, and Hypocreales, with additional contributions from Capnoidales and Agaricales (Fig. 1B). Similar fungal groups have been identified as dominant components of outdoor aerobiomes in tropical and subtropical regions^{2,25,26}.

To enhance taxonomic resolution, we generated genus-level heatmaps using taxa with a mean relative abundance greater than 0.1% (Fig. 2). The bacterial communities (Fig. 2A) featured widespread genera such as

Massilia, *Methylobacterium*-*Methylorubrum*, *Sphingomonas*, *Pseudomonas*, *Bacillus*, *Kocuria*, *Micrococcus*, *Staphylococcus*, and *Paenibacillus*. Likewise, fungal communities (Fig. 2B) were dominated by *Cladosporium*, *Alternaria*, *Aspergillus*, *Curvularia*, and *Penicillium*. These genera were found across multiple countries but exhibited variations in relative abundance, demonstrating spatial heterogeneity at finer taxonomic levels. The prevalence of *Cladosporium* and *Alternaria* aligns with previous aerobiological studies in Africa, including Senegal, where these genera were reported among the dominant fungal taxa in outdoor air^{26–28}.

The genus-level analyses also underscored the significance of low-abundance taxa in shaping airborne microbial communities. Genera with mean relative abundances below 0.1% collectively accounted for approximately 32–46% of the bacterial community and 34–55% of the fungal community, indicating that a substantial portion of the regional aerobiome comprises rare taxa. These findings highlight that East African airborne microbial communities consist of both widely distributed dominant taxa and a diverse assemblage of less abundant microorganisms, consistent with previous observations that atmospheric microbial communities are derived from multiple environmental reservoirs and land-use types^{6,18,23,29}.

Although many dominant bacterial and fungal taxa were shared among locations, their relative abundances varied significantly between land-use types^{18,22,28,30}. Comparisons of neighboring cross-border sites revealed differences in microbial composition despite their close geographic proximity. Although cross-border locations shared many dominant bacterial classes, fungal orders, and genera, variations in their relative abundances were observed. This pattern was particularly evident in the Goma–Rubavu and Bukavu–Rusizi site pairs, which are separated by less than 10 km but displayed distinct microbial signatures. These findings suggest that geographic proximity alone is insufficient to predict similarity in airborne microbial composition^{2,6,31–34}.

Overall, the taxonomic patterns demonstrate that East African airborne microbial communities share a common regional taxonomic core comprising dominant bacterial classes, fungal orders, and widely distributed genera. However, variations in the relative abundance of these taxa among countries and neighboring border locations highlight spatial heterogeneity in community composition. Together, these findings support the presence of a broadly shared East African aerobiome while emphasizing localized compositional differences across border regions.

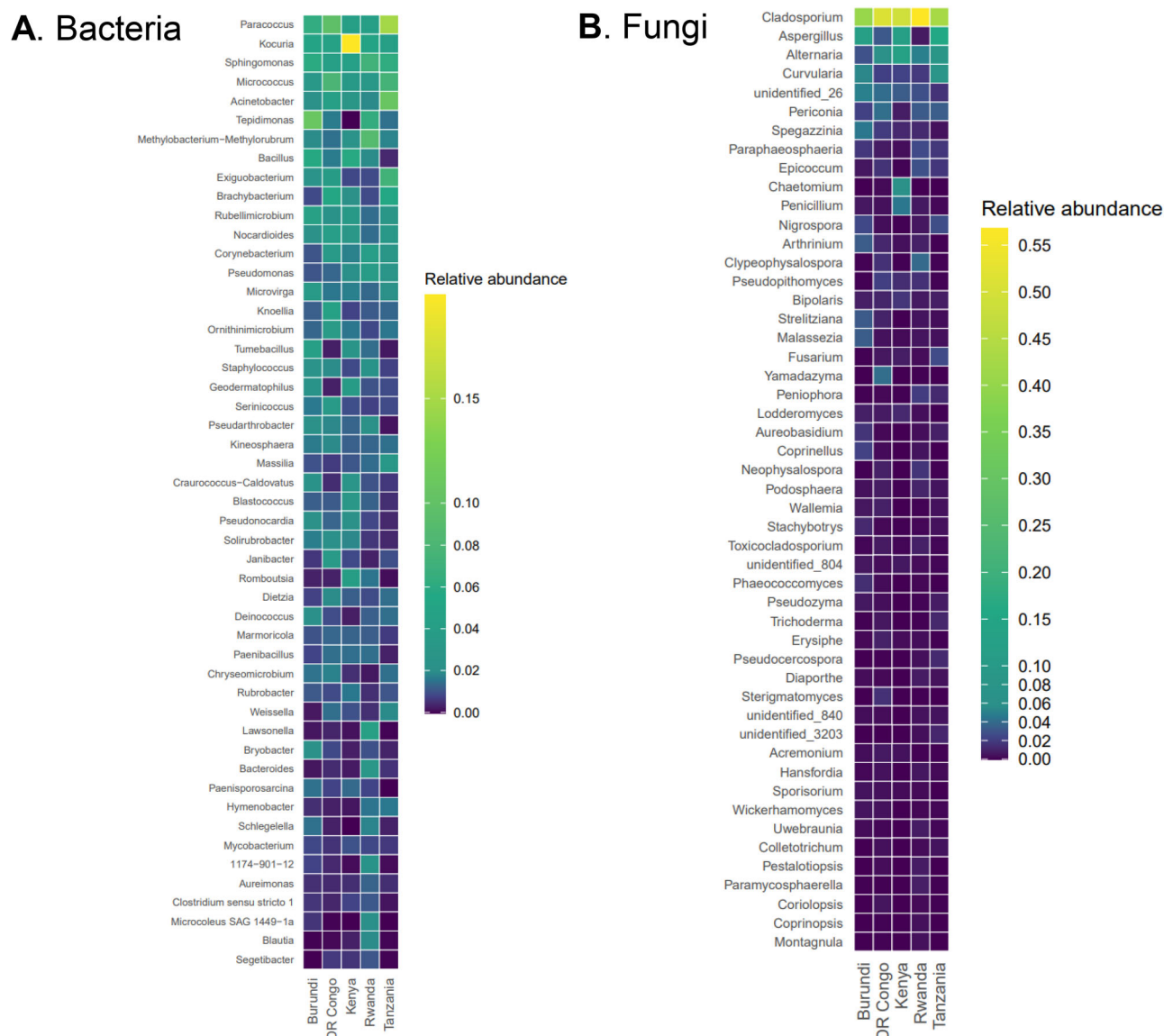


Fig. 2 | Heatmaps showing the relative abundance of the top 50 genera detected in this study. The bacterial (16S rRNA gene, **A**) and fungal (ITS, **B**) genera in East African bioaerosol samples, aggregated by country. Genera were ranked by mean relative abundance across all East African samples, excluding unclassified genera, and the 50 most abundant are displayed. Abundances were averaged within each

country (Burundi, DR Congo, Kenya, Rwanda, Tanzania) following normalisation to relative abundance. Genera are ordered along the y-axis by increasing mean relative abundance from bottom to top, with the most abundant genus appearing at the top. Colour intensity reflects relative abundance on a non-linear viridis scale with finer resolution below 10% to aid visualisation of low-abundance taxa.

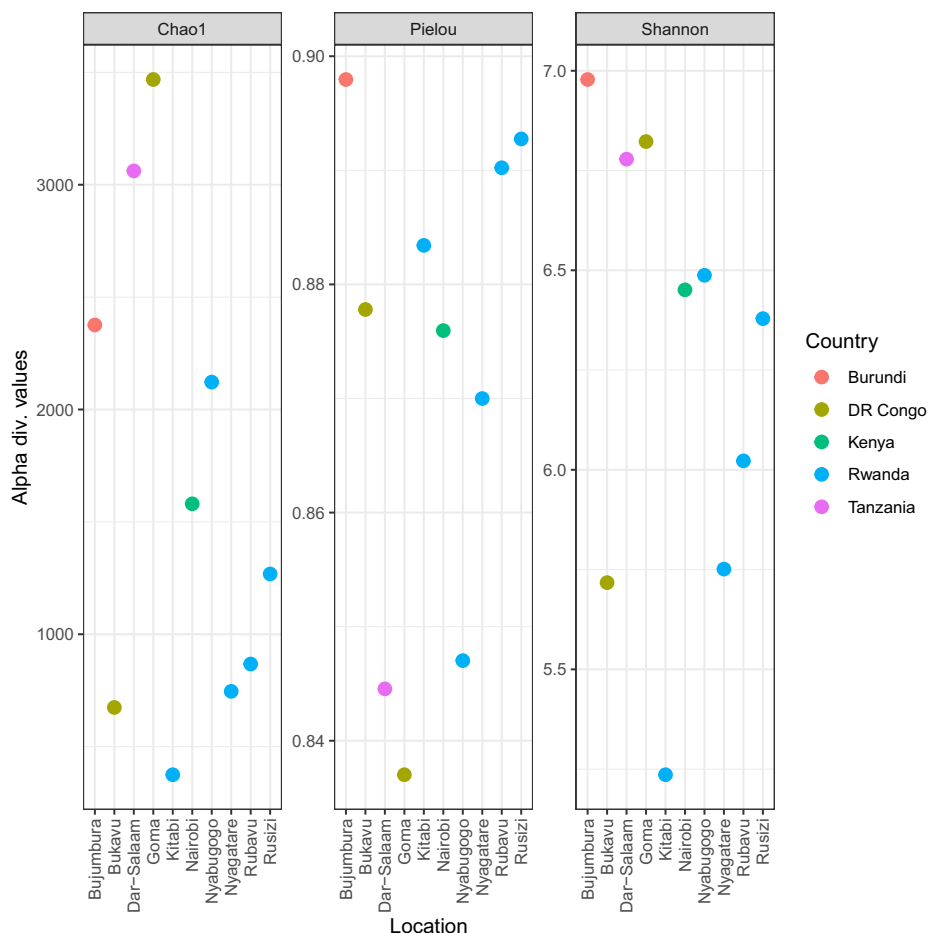
Spatial patterns of airborne microbial diversity

Airborne bacterial and fungal communities exhibited significant spatial variation in richness (Chao 1) and Pielou's evenness across East African sampling sites³⁵. Airborne bacterial communities consistently exhibited higher richness, evenness, and diversity compared to fungal communities across the sampled locations (Fig. 3). The Chao1 richness values for bacteria varied significantly among sites, with the highest richness recorded in the Democratic Republic of the Congo (DRC) and Tanzania, while Pielou's evenness remained relatively high across most samples. In contrast, fungal communities (Fig. 4) demonstrated lower overall richness and diversity; however, certain sites in Rwanda showed comparatively high fungal richness.

These findings align with previous studies, which indicate that bacteria and fungi display distinct diversity patterns, reflecting differences in their atmospheric ecology and dispersal characteristics^{5,9,23}. Nevertheless, due to the limited replication at several locations, these patterns should be regarded as descriptive observations rather than evidence of statistically significant

differences among countries or environmental contexts. Therefore, the diversity analyses provide a foundational overview of airborne microbial diversity across East Africa and complement the community composition analyses. Generally, bacterial communities exhibited greater richness and evenness than their fungal counterparts at most locations⁵. Notable variability was observed among sites, with Goma exhibiting the highest bacterial richness and Kitabi the lowest, but Kitabi displayed the highest fungal richness⁹. Rubavu and Rusizi showed intermediate diversity values²³. Interestingly, neighboring cross-border locations, such as Goma–Rubavu and Bukavu–Rusizi, exhibited distinct diversity patterns despite being separated by less than 10 km⁶. These findings highlight substantial spatial heterogeneity in airborne microbial diversity throughout the study region and suggest that geographic proximity alone does not reliably predict similarities in microbial community diversity^{1,36}. The observed diversity patterns reflect the influence of local environmental conditions, land use, vegetation cover, urbanization, and atmospheric processes^{9,18,29}. Across most locations, bacterial communities exhibited higher richness and Pielou's

Fig. 3 | Alpha diversity of country-level comparison of bacteria across five East African countries. Species richness (Chao1) and community evenness (Pielou's and Shannon) were analyzed across 10 sites: Bujumbura (Burundi); Bukavu and Goma (DRC); Nairobi (Kenya); Dar es Salaam (Tanzania); and Kitabi, Nyagatare, Nyabugogo, Rusizi, and Rubavu (Rwanda).



evenness than fungal communities, indicating notable differences in community structure^{37,38}. While these diversity metrics describe community complexity and taxonomic distribution, they do not necessarily imply differences in microbial abundance or viability³⁹. The patterns observed suggest that airborne bacterial communities are broadly distributed across various environments, including urban centers, transportation corridors, coastal regions, and areas influenced by volcanic activity^{17,22,24,31,34}. In contrast, fungal diversity appeared more closely associated with vegetation-rich environments^{5,8,40}. For example, Kitabi, situated within Nyungwe National Park, exhibited the highest fungal richness among all sampled sites, consistent with its role as a critical reservoir for airborne fungal taxa^{32,38}. This observation aligns with previous studies indicating that vegetation cover and ecosystem type are significant determinants of atmospheric fungal community structure.

To evaluate whether spatial proximity influences similarity in airborne microbial communities, we examined paired cross-border sites located within approximately 10 km of each other²⁹. Despite their geographic closeness, the Goma–Rubavu and Bukavu–Rusizi pairs displayed noticeable differences in both bacterial and fungal diversity^{18,34}. These findings suggest that short geographic distances do not necessarily result in similar airborne microbial communities. Instead, local environmental factors such as land cover, urban development, vegetation, volcanic influence, and atmospheric mixing appear to play a more critical role in shaping microbial diversity than political boundaries or spatial proximity^{6,22,24,31,41}. The variability observed between neighboring sites highlights the responsiveness of airborne microbial communities to local ecological conditions and sampling type^{19,41}. For instance, locations characterized by intense human activity, transportation, or volcanic influences tended to support diverse bacterial assemblages, while areas with substantial vegetation cover fostered richer fungal communities^{38,42}. Such

patterns are consistent with the diverse environmental sources contributing microorganisms to the atmosphere, including soil, vegetation, water bodies, volcanoes and human-associated activities^{25,43–45}.

Overall, the findings suggest that airborne microbial diversity across East Africa is primarily structured by local environmental conditions rather than by country-level characteristics or geographic distance alone⁴⁴. The lack of consistent similarity among nearby cross-border locations highlights the importance of considering site-specific ecological factors when evaluating aerobiome dynamics⁵. These observations further emphasize the need for localized monitoring strategies to enhance our understanding of airborne microbial communities and their potential implications for environmental quality, ecosystem functioning, and human exposure in rapidly changing East African environments.

Community structure

Principal Coordinates Analysis (PCoA) was used to assess differences in airborne bacterial and fungal community composition across various countries (Fig. 5). The ordination of bacterial communities revealed substantial overlap among countries, with samples from different locations clustering in similar areas of the ordination space (Fig. 5A). This finding was corroborated by ANOSIM, which indicated no significant differences in bacterial community composition among countries ($R = -0.045$, $p = 0.597$). These results suggest that bacterial communities were broadly similar throughout the study region, despite variations in local environmental conditions. Comparable patterns of extensive bacterial dispersal and weak geographic structuring have been documented in atmospheric microbiome studies conducted at both regional and continental scales^{6,9,25,29}. In contrast, fungal communities displayed more distinct clustering by country (Fig. 5B). ANOSIM confirmed significant differences in fungal

Fig. 4 | Alpha diversity of country-level comparison of fungi across five East African countries. Species richness (Chao1) and community evenness (Pielou's and Shannon) were analyzed across 10 sites: Bujumbura (Burundi); Bukavu and Goma (DRC); Nairobi (Kenya); Dar es Salaam (Tanzania); and Kitabi, Nyagatare, Nyabugogo, Rusizi, and Rubavu (Rwanda).

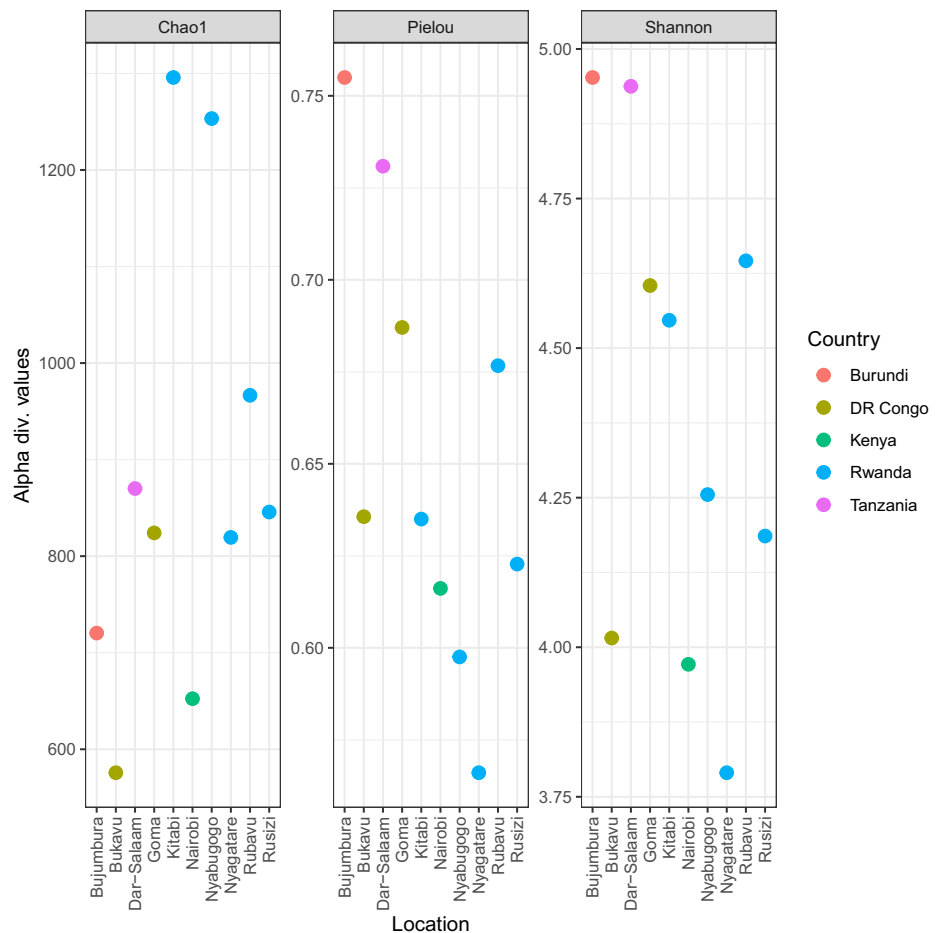
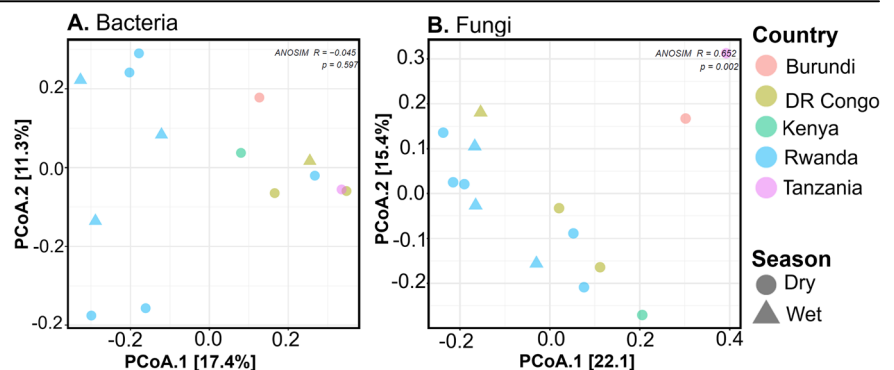


Fig. 5 | Principal Coordinates Analysis (PCoA) of airborne microorganism. PCoA of bacterial (A) and fungal (B) communities across East African countries, based on Bray–Curtis dissimilarity. The analysis revealed no significant country-level differences in bacterial communities (ANOSIM ($R = -0.045$, $p = 0.597$)), while fungal communities exhibited significant differences among countries (ANOSIM ($R = 0.652$, $p = 0.002$)). Colors represent different countries, and symbols indicate the duration of sampling.



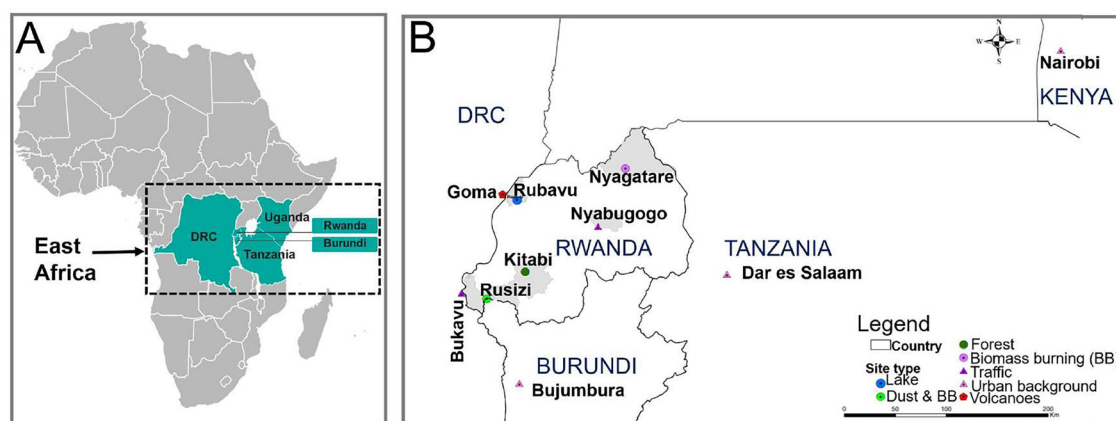
community composition among countries ($R = 0.652$, $p = 0.002$), indicating stronger geographic structuring of fungal communities than of their bacterial counterparts. The observed separation in the ordination suggests that fungal assemblages varied more consistently across countries, while bacterial communities were relatively homogeneous throughout the region. Previous studies have similarly reported that fungal communities tend to exhibit stronger spatial and environmental structuring than bacterial communities, as fungal dispersal and establishment are often more closely linked to local vegetation, climate, and landscape characteristics^{5,22,38,46}. The contrasting patterns observed for bacteria and fungi align with broader findings that different microbial groups exhibit distinct biogeographic patterns in the atmosphere^{4,9,10}. Overall, the beta-diversity analyses indicate that country-level differences were more pronounced for fungal than for

bacterial communities, reinforcing the conclusion that fungal community composition exhibited stronger spatial structuring across East Africa, whereas bacterial communities appeared to form a more homogeneous regional aerobiome.

This study is the first regional-scale characterization of airborne bacterial and fungal communities across multiple East African countries, using polyurethane foam passive air samplers (PUF-PASs) and culture-independent sequencing methods. The airborne microbial communities were predominantly composed of a shared set of bacterial classes, fungal orders, and widely distributed genera, with notable differences in taxonomic composition observed among sampling locations. Genus-level analyses revealed spatial heterogeneity in community composition, with neighboring cross-border sites separated by less than 10 km often exhibiting distinct microbial

Table 1 | Summary of the site description, coordinates and altitude of the study site using Polyurethane foam passive air samplers (PUF-PASs)

Site, City	Latitude (°S)	Longitude (°E)	Altitude (m)	Total volume	Site Characteristics
Nyabugogo, Rwanda	−1.94	30.04	1,460	120 m ³	Kigali urban basin: major traffic hub
Nyagatare, Rwanda	−1.3	30.31	1,410	120 m ³	Eastern lowlands, near the Uganda border
Kitabi, Rwanda	−2.6	29.55	2,370	120 m ³	High-altitude site near Nyungwe forest
Rusizi, Rwanda	−2.48	28.9	900	120 m ³	Western lowland, near the Lake Kivu border
Rubavu, Rwanda	−1.7	29.25	1460	120 m ³	Lakeside border city with Goma
Bukavu, RD Congo	−2.51	28.86	1500	120 m ³	Hill City on Lake Kivu's southern shore
Goma, RD Congo	−1.67	29.22	1470	120 m ³	Volcanic plateau near Nyiragongo
Bujumbura, Burundi	−3.38	29.36	780	120 m ³	On the shore of Lake Tanganyika
Dar-es-Salaam, Tanzania	−6.79	39.2	57.0	120 m ³	Coastal, sea-level city
Nairobi, Kenya	−1.28	36.81	1795	240 m ³	Highland capital, central plateau

**Fig. 6 | Study area and sampling locations in East Africa. A** Geographic locations of the five study countries within Africa. **B** Sampling sites and their dominant emission sources or environmental characteristics: Nyabugogo, Rwanda (traffic); Nyagatare, Rwanda (wood burning); Rusizi, Rwanda (rural dust and biomass burning); Kitabi, Rwanda (rural forest); Rubavu, Rwanda (lake environment); Bujumbura, Burundi (urban background); Dar es Salaam, Tanzania (urban

background); Goma, Democratic Republic of the Congo (volcanic emissions); Bukavu, Democratic Republic of the Congo (traffic); and Nairobi, Kenya (traffic). Panel A was created by the authors using BioRender.com. Panel B was produced by the authors using ArcGIS Desktop version 10.8 (Esri, Redlands, CA, USA), in accordance with Esri's terms of use for publication.

signatures. This finding suggests that geographic proximity alone does not reliably predict similarity in airborne microbial communities. This study demonstrates that PUF-PAS, which is inexpensive and requires no intensive maintenance or electricity to operate, could be used as an alternative tool for characterizing air pollution and for surveillance networks in low-resource settings in Africa lacking conventional air monitoring infrastructure.

The study was based on a relatively small sample size and limited replication across locations, which limits the statistical power to assess regional differences in microbial diversity. Data were collected only in a single city and for a single season; future studies incorporating greater temporal replication across multiple cities, seasonal sampling, and broader geographic coverage will be crucial for a comprehensive understanding of the environmental drivers and dynamics of airborne microbial communities across Africa. Research comparing passive sampling with active methods in diverse environments and sampling durations will provide a more robust evaluation of performance. Future studies should compare both active and passive air samplers for characterization of bioaerosols in the East African region, and these studies will be vital in refining best practices for large-scale airborne microbial monitoring in Africa and other resource-limited regions. Additionally, the 16S rRNA V4 and ITS amplicon sequencing approaches provide limited taxonomic resolution and do not consistently support species-level identification or direct functional inference. Therefore, the results should be viewed primarily as a descriptive baseline assessment of airborne microbial community composition.

Methods

Sampling sites and sampling design

Ten sampling sites were selected across five East African countries (Table 1 and Fig. 6). These sites included densely populated cities (Nairobi, Kenya and Dar es Salaam, Tanzania), volcanic zones (Goma, Democratic Republic of the Congo (DRC)), lakeside regions (Rubavu and Rusizi, Rwanda), urban residential areas (Bujumbura, Burundi), remote forests (Kitabi in Rwanda), traffic corridors (Nyabugogo, Rwanda and Bukavu in DRC), and arid environment rural residential areas (Nyagatare, Rwanda). Special attention was paid to close-proximity cross-border cities (Rubavu-Goma and Rusizi-Bukavu). The total number of monthly samples ($n = 10$) was collected across all countries, including Rwanda ($n = 5$), DRC ($n = 2$), Burundi ($n = 1$), Kenya ($n = 1$), and Tanzania ($n = 1$). PUF disks were positioned horizontally in pre-cleaned stainless-steel chambers. Immediately after field deployment, all samples were stored at 4 °C and transported to the laboratory under refrigerated conditions^{22,41}. Prior to extraction, PUF samples were maintained in pre-cleaned, solvent-rinsed glass jars to minimize the risk of contamination. For QA/QC purposes, two field blanks were incorporated throughout the sampling campaign. Each field blank consisted of sterile sampling media that were transported to the sampling site, inserted into the sampler, and briefly exposed to ambient air for a few seconds. These blank media were subsequently removed, stored, and processed in the same manner as environmental samples, including DNA extraction, library preparation, sequencing, and PCR. The blanks were used to assess potential

contamination arising from sample handling, transport, field exposure, laboratory processing, and molecular workflows. All laboratory consumables and sampling containers were pre-cleaned before use, and extraction procedures were performed using sterile techniques in a contamination-controlled laboratory to minimize analytical bias.

PUF-PASs (14 cm diameter × 1.35 cm thick, surface area 365 cm², mass 4.40 g, volume 207 cm³, PUF-PAS, Tisch Environmental, TE-200-PAS, Cleves, USA) (Fig. 1B) were simultaneously deployed for 30 days during the dry season (June–July 2024) at each site. PUF-PASs were mounted 2 to 3 metres above the ground in the open air at each site. PUF-PASs collected gas and particle species (<5 µm) into the white PUF-DISK foam, which changes colour after exposure to ambient air due to particle deposition and atmospheric oxidants, resulting in a yellowing of the PUF surface. PUF-PASs have an average air sampling rate of approximately 4 m³/day²². A detailed description of PUF-PASs was provided in our previous study²². Field blanks (*n* = 2) were also collected along with the samples by exposing PUF disks to air for 1 min²².

DNA extraction and sequencing analysis

Genomic DNA was isolated from PUF-PAS samples using the DNeasy PowerMax Soil Kit (Qiagen), following the manufacturer's instructions and details are provided in our previous studies^{22,41}. Each PUF-disk sample was divided into six equal segments prior to DNA extraction²². The extraction of each of these six segments was conducted separately, following the protocol outlined in the PowerMax Soil DNA Isolation Kit (Qiagen, USA). The resulting extracts were then combined and transferred to a PowerMax Bead Tube for cell lysis and subsequent DNA extraction. This process enabled the recovery of particulate matter and associated microorganisms from the polyurethane foam material before DNA purification. The purified DNA was eluted from the Maxi Spin Column in 5 mL of Solution C6 and stored at −20 °C until PCR amplification. Filter blanks and PUF blanks were processed in the same manner as the field samples to ensure consistency. A schematic overview of the DNA extraction workflow is provided in our previous study²².

DNA quantity and quality were determined using a NanoDrop2000 (Thermo Scientific). The 16S rRNA gene V4 variable region PCR primers 515/806 were used in a 30–35 cycle (depending on primers and DNA), and the ITS1 fungal region.

The genomic DNA analysis was conducted using the AllTaq Master Mix Kit (Qiagen, USA) under the following conditions: 95 °C for 5 min, followed by 30–35 cycles of 95 °C for 30 s, 53 °C for 40 s, and 72 °C for 1 min, after which a final elongation step at 72 °C for 10 minutes was performed. After amplification, PCR products were visualized on a 2% agarose gel to assess amplification success and band intensities. The total bacterial (16r RNA gene abundance was quantified using the following primer-probe set: Bacteria-Updated sequences: 515F⁴⁷–806R⁴⁸, forward-barcode: (FWD:GTGYCAGCMGCCGCGGTAA; REV:GGAC-TACNVGGGTWTCTAAT) and for fungi, the internal transcribed spacer region (~400 bp) of fungal 18S and 5.8S RNA genes (ITS1 forward and ITS2 reverse)^{22,41}. Sequence libraries were prepared from the amplicons using the Illumina MiSeq platform (at Molecular Research LP (MRDNA, Shallowater TX, USA), following the manufacturer's protocol. Libraries were first processed with cutadapt v4.8⁴⁹ to remove primer sequences, then with the R package dada2 v1.26⁵⁰ to generate amplicon sequence variants (ASVs)^{50,51}. In DADA2, reads were trimmed to uniform lengths of 185 bp (forward) and 140 bp (reverse), and reads exceeding 2 expected errors (forward) or 5 (reverse) were discarded. Pseudo-pooling was used during ASV calling to increase sensitivity and improve detection of rare ASVs. Taxonomic classification was performed in DADA2 against the SILVA v138.1 database⁵². Alpha diversity indices, determined using Chao 1, Pielou and Shannon metrics, were computed to evaluate richness and diversity. Relative abundance was calculated as the proportion of sequence reads assigned to a specific taxon compared to the total number of quality-filtered reads within each sample and is reported as a percentage. Community composition was

depicted by Principal Coordinate Analysis (PCoA) using Bray–Curtis dissimilarity matrices (95% Confidence interval)⁵³, and ANOSIM R-values were calculated to assess the degree of dissimilarity among groups.

Sequence data were processed using the MR DNA analysis pipeline (MR DNA, Shallowater, TX, USA)⁴¹. We sequenced the 16S rRNA (V4 region) and ITS fungal region using an Illumina MiSeq at MR DNA (Shallowater, TX, USA) following the manufacturer's guidelines. Further details on the bioinformatic method are described in our recent studies^{22,41}. All analyses were performed using the R package phyloseq v1.51.0⁵⁴, and data visualization was performed using ggplot2 v4.0.1⁵⁵.

Data availability

All sequencing reads used for this study were deposited in the EMBL-EBI European Nucleotide Archive (ENA) and publicly available under the study accession number: ERP177853.

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E.K.: Conceptualization, data curation, formal analysis, visualization, methodology, writing-original draft, writing-review & edits. T.H., A.S., M.A., F.o.P., K.L., S.P., A.N., T.N., A.S. and J.M.: Conceptualization, Methodology, writing-review & edits Y.U. and F.K.: Data collection in East African Cities.

Competing interests

The authors declare no competing interests.

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